

#11



Pct/10

## RAW SEQUENCE LISTING

DATE: 08/08/2002

PATENT APPLICATION: US/10/031,021

TIME: 23:58:21

Input Set : N:\Crf3\08062002\J031021.raw

Output Set: N:\CRF4\08082002\J031021.raw

1 <110> APPLICANT: GABANT, Philippe  
 2 ROSCAM-SZPIRER, Josiane  
 3 <120> TITLE OF INVENTION: NON-HUMAN GENETICALLY MODIFIED MAMMAL LACKING THE ALPHA-FETOPROTEIN  
 4 <130> FILE REFERENCE: VANM243.1APC1  
 5 <140> CURRENT APPLICATION NUMBER: US/10/031,021  
 6 <141> CURRENT FILING DATE: 2002-01-14  
 7 <150> PRIOR APPLICATION NUMBER: PCT/BE00/00081  
 8 <151> PRIOR FILING DATE: 2000-07-11  
 9 <160> NUMBER OF SEQ ID NOS: 8  
 10 <170> SOFTWARE: PatentIn version 3.1  
 12 <210> SEQ ID NO: 1  
 13 <211> LENGTH: 31  
 14 <212> TYPE: DNA  
 15 <213> ORGANISM: Artificial Sequence  
 16 <220> FEATURE:  
 17 <223> OTHER INFORMATION: N-Mer1 primer  
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 25 <220> FEATURE:  
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 33 <213> ORGANISM: Artificial Sequence  
 34 <220> FEATURE:  
 35 <223> OTHER INFORMATION: Description of Artificial Sequence: afp#1 primer  
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 39 <210> SEQ ID NO: 4  
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 45 <400> SEQUENCE: 4  
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 48 <210> SEQ ID NO: 5

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50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
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60 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
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67 <211> LENGTH: 2009
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71 <221> NAME/KEY: CDS
72 <222> LOCATION: (42)..(1856)
73 <223> OTHER INFORMATION:
74 <400> SEQUENCE: 7
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76                                     Met Lys Trp Ile Thr
77                                     1           5
78     ccc gct tcc ctc atc ctc ctg cta cat ttc gct gcg tcc aaa gca ttg    104
79     Pro Ala Ser Leu Ile Leu Leu Leu His Phe Ala Ala Ser Lys Ala Leu
80             10             15             20
81     cac gaa aat gag ttt ggg ata gct tcc acg tta gat tcc tcc cag tgc    152
82     His Glu Asn Glu Phe Gly Ile Ala Ser Thr Leu Asp Ser Ser Gln Cys
83             25             30             35
84     gtg acg gag aag aat gtg ctt agc ata gct acc atc acc ttt acc cag    200
85     Val Thr Glu Lys Asn Val Leu Ser Ile Ala Thr Ile Thr Phe Thr Gln
86             40             45             50
87     ttt gtt ccg gaa gcc acc gag gag gaa gtg aac aaa atg act agc gat    248
88     Phe Val Pro Glu Ala Thr Glu Glu Glu Val Asn Lys Met Thr Ser Asp
89             55             60             65
90     gtg ttg gct gca atg aag aaa aac tct ggc gat ggg tgt tta gaa agc    296
91     Val Leu Ala Ala Met Lys Lys Asn Ser Gly Asp Gly Cys Leu Glu Ser
92     70             75             80             85
93     cag cta tct gtg ttt ctg gat gaa att tgc cat gag acg gaa ctc tct    344
94     Gln Leu Ser Val Phe Leu Asp Glu Ile Cys His Glu Thr Glu Leu Ser
95             90             95             100
96     aac aag tat gga ctc tca ggc tgc tgc agc caa agt gga gtg gaa aga    392
97     Asn Lys Tyr Gly Leu Ser Gly Cys Cys Ser Gln Ser Gly Val Glu Arg
98             105             110             115
99     cat cag tgt ctg ctg gca cgc aag aag act gct ccg gcc tct gtc cca    440

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100	His	Gln	Cys	Leu	Leu	Ala	Arg	Lys	Lys	Thr	Ala	Pro	Ala	Ser	Val	Pro	
101			120					125					130				
102	ccc	ttc	cag	ttt	cca	gaa	cct	gcc	gag	agt	tgc	aaa	gca	cat	gaa	gaa	488
103	Pro	Phe	Gln	Phe	Pro	Glu	Pro	Ala	Glu	Ser	Cys	Lys	Ala	His	Glu	Glu	
104		135					140				145						
105	aac	agg	gca	gtg	ttc	atg	aac	agg	ttc	atc	tat	gaa	gtg	tca	agg	agg	536
106	Asn	Arg	Ala	Val	Phe	Met	Asn	Arg	Phe	Ile	Tyr	Glu	Val	Ser	Arg	Arg	
107	150					155				160						165	
108	aac	ccc	ttc	atg	tat	gcc	cca	gcc	att	ctg	tcc	ttg	gct	gct	cag	tac	584
109	Asn	Pro	Phe	Met	Tyr	Ala	Pro	Ala	Ile	Leu	Ser	Leu	Ala	Ala	Gln	Tyr	
110				170						175					180		
111	gac	aag	gtc	gtt	ctg	gca	tgc	tgc	aaa	gct	gac	aac	aag	gag	gag	tgc	632
112	Asp	Lys	Val	Val	Leu	Ala	Cys	Cys	Lys	Ala	Asp	Asn	Lys	Glu	Glu	Cys	
113			185						190				195				
114	ttc	cag	aca	aag	aga	gca	tcc	att	gca	aag	gaa	tta	aga	gaa	gga	agc	680
115	Phe	Gln	Thr	Lys	Arg	Ala	Ser	Ile	Ala	Lys	Glu	Leu	Arg	Glu	Gly	Ser	
116		200					205				210						
117	atg	tta	aat	gag	cat	gta	tgt	tca	gtg	ata	aga	aaa	ttt	gga	tcc	cga	728
118	Met	Leu	Asn	Glu	His	Val	Cys	Ser	Val	Ile	Arg	Lys	Phe	Gly	Ser	Arg	
119		215					220				225						
120	aac	ctc	cag	gca	aca	acc	att	att	aag	cta	agt	caa	aag	tta	act	gaa	776
121	Asn	Leu	Gln	Ala	Thr	Thr	Ile	Ile	Lys	Leu	Ser	Gln	Lys	Leu	Thr	Glu	
122	230				235					240					245		
123	gca	aat	ttt	act	gag	att	cag	aag	ctg	gcc	ctg	gat	gtg	gct	cac	atc	824
124	Ala	Asn	Phe	Thr	Glu	Ile	Gln	Lys	Leu	Ala	Leu	Asp	Val	Ala	His	Ile	
125			250						255				260				
126	cac	gag	gag	tgt	tgc	caa	gga	aac	tcg	ctg	gag	tgt	ctg	cag	gat	ggg	872
127	His	Glu	Glu	Cys	Gln	Gly	Asn	Ser	Leu	Glu	Cys	Leu	Gln	Asp	Gly		
128			265					270					275				
129	gaa	aaa	gtc	atg	aca	tat	ata	tgt	tct	caa	caa	aat	att	ctg	tca	agc	920
130	Glu	Lys	Val	Met	Thr	Tyr	Ile	Cys	Ser	Gln	Gln	Asn	Ile	Leu	Ser	Ser	
131		280					285					290					
132	aaa	ata	gca	gag	tgc	tgc	aaa	tta	ccc	atg	atc	caa	cta	ggc	ttc	tgc	968
133	Lys	Ile	Ala	Glu	Cys	Cys	Lys	Leu	Pro	Met	Ile	Gln	Leu	Gly	Phe	Cys	
134		295				300				305							
135	ata	att	cac	gca	gag	aat	ggc	gtc	aaa	cct	gaa	ggc	tta	tct	cta	aat	1016
136	Ile	Ile	His	Ala	Glu	Asn	Gly	Val	Lys	Pro	Glu	Gly	Leu	Ser	Leu	Asn	
137	310				315				320				325				
138	cca	agc	cag	ttt	ttg	gga	gac	aga	aat	ttt	gcc	caa	ttt	tct	tca	gag	1064
139	Pro	Ser	Gln	Phe	Leu	Gly	Asp	Arg	Asn	Phe	Ala	Gln	Phe	Ser	Ser	Glu	
140			330						335				340				
141	gaa	aaa	atc	atg	ttc	atg	gca	agc	ttt	ctt	cat	gaa	tac	tca	aga	act	1112
142	Glu	Lys	Ile	Met	Phe	Met	Ala	Ser	Phe	Leu	His	Glu	Tyr	Ser	Arg	Thr	
143			345					350				355					
144	cac	ccc	aac	ctt	cct	gtc	tca	gtc	att	cta	aga	att	gct	aaa	acg	tac	1160
145	His	Pro	Asn	Leu	Pro	Val	Ser	Val	Ile	Leu	Arg	Ile	Ala	Lys	Thr	Tyr	
146		360						365				370					
147	cag	gaa	ata	ttg	gag	aag	tgt	tcc	cag	tct	gga	aat	cta	cct	gga	tgt	1208
148	Gln	Glu	Ile	Leu	Glu	Lys	Cys	Ser	Gln	Ser	Gly	Asn	Leu	Pro	Gly	Cys	

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149	375	380	385	
150	cag gac aat ctg gaa gaa gaa ttg cat aaa cac atc gag gag agc cag	1256		
151	Gln Asp Asn Leu Glu Glu Glu Leu His Lys His Ile Glu Glu Ser Gln			
152	390 395 400 405			
153	gca ctg tcc aag caa agc tgc gct ctc tac cag acc tta gga gac tac	1304		
154	Ala Leu Ser Lys Gln Ser Cys Ala Leu Tyr Gln Thr Leu Gly Asp Tyr			
155	410 415 420			
156	aaa tta caa aat ctg ttc ctt att ggt tac acg agg aaa gcc cct cag	1352		
157	Lys Leu Gln Asn Leu Phe Leu Ile Gly Tyr Thr Arg Lys Ala Pro Gln			
158	425 430 435			
159	ctg acc tca gca gag ctg atc gac ctc acc ggg aag atg gtg agc att	1400		
160	Leu Thr Ser Ala Glu Leu Ile Asp Leu Thr Gly Lys Met Val Ser Ile			
161	440 445 450			
162	gcc tcc acg tgc tgc cag ctc agc gag gag aaa tgg tcc ggc tgt ggt	1448		
163	Ala Ser Thr Cys Cys Gln Leu Ser Glu Glu Lys Trp Ser Gly Cys Gly			
164	455 460 465			
165	gag gga atg gcc gac att ttc att gga cat ttg tgt ata agg aat gaa	1496		
166	Glu Gly Met Ala Asp Ile Phe Ile Gly His Leu Cys Ile Arg Asn Glu			
167	470 475 480 485			
168	gca agc cct gtg aac tct ggt atc agc cac tgc tgc aac tct tcg tat	1544		
169	Ala Ser Pro Val Asn Ser Gly Ile Ser His Cys Cys Asn Ser Ser Tyr			
170	490 495 500			
171	tcc aac agg agg cta tgc atc acc agt ttt ctg agg gat gaa acc tat	1592		
172	Ser Asn Arg Arg Leu Cys Ile Thr Ser Phe Leu Arg Asp Glu Thr Tyr			
173	505 510 515			
174	gcc cct ccc cca ttc tct gag gat aaa ttc atc ttc cac aag gat ctg	1640		
175	Ala Pro Pro Pro Phe Ser Glu Asp Lys Phe Ile Phe His Lys Asp Leu			
176	520 525 530			
177	tgc caa gct cag ggc aaa gcc cta cag acc atg aaa caa gag ctt ctc	1688		
178	Cys Gln Ala Gln Gly Lys Ala Leu Gln Thr Met Lys Gln Glu Leu Leu			
179	535 540 545			
180	att aac ctg gtg aag caa aag cct gaa ctg aca gag gag cag ctg gcg	1736		
181	Ile Asn Leu Val Lys Gln Lys Pro Glu Leu Thr Glu Glu Gln Leu Ala			
182	550 555 560 565			
183	gct gtc act gca gat ttc tcg ggc ctt ttg gag aag tgc tgc aaa gcc	1784		
184	Ala Val Thr Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Lys Ala			
185	570 575 580			
186	cag gac cag gaa gtc tgt ttc aca gaa gag ggt cca aag ttg att tcc	1832		
187	Gln Asp Gln Glu Val Cys Phe Thr Glu Glu Gly Pro Lys Leu Ile Ser			
188	585 590 595			
189	aaa act cgt gat gct ttg ggc gtt taaacatctc cagaaggaag agtggacaaa	1886		
190	Lys Thr Arg Asp Ala Leu Gly Val			
191	600 605			
192	aaaatgtgtt gacgcttttg tgtgagcctt ttggcttaac tgtaactgct agtactttaa	1946		
193	ccacatggtg aagatgtcca tgtgagatit ctatacctta ggaataaaaa cttttcaact	2006		
194	att	2009		
196	<210> SEQ ID NO: 8			
197	<211> LENGTH: 605			
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199 <213> ORGANISM: Apodemus
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201 Met Lys Trp Ile Thr Pro Ala Ser Leu Ile Leu Leu Leu His Phe Ala
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204 20 25 30
205 Asp Ser Ser Gln Cys Val Thr Glu Lys Asn Val Leu Ser Ile Ala Thr
206 35 40 45
207 Ile Thr Phe Thr Gln Phe Val Pro Glu Ala Thr Glu Glu Glu Val Asn
208 50 55 60
209 Lys Met Thr Ser Asp Val Leu Ala Ala Met Lys Lys Asn Ser Gly Asp
210 65 70 75 80
211 Gly Cys Leu Glu Ser Gln Leu Ser Val Phe Leu Asp Glu Ile Cys His
212 85 90 95
213 Glu Thr Glu Leu Ser Asn Lys Tyr Gly Leu Ser Gly Cys Cys Ser Gln
214 100 105 110
215 Ser Gly Val Glu Arg His Gln Cys Leu Leu Ala Arg Lys Lys Thr Ala
216 115 120 125
217 Pro Ala Ser Val Pro Pro Phe Gln Phe Pro Glu Pro Ala Glu Ser Cys
218 130 135 140
219 Lys Ala His Glu Glu Asn Arg Ala Val Phe Met Asn Arg Phe Ile Tyr
220 145 150 155 160
221 Glu Val Ser Arg Arg Asn Pro Phe Met Tyr Ala Pro Ala Ile Leu Ser
222 165 170 175
223 Leu Ala Ala Gln Tyr Asp Lys Val Val Leu Ala Cys Cys Lys Ala Asp
224 180 185 190
225 Asn Lys Glu Glu Cys Phe Gln Thr Lys Arg Ala Ser Ile Ala Lys Glu
226 195 200 205
227 Leu Arg Glu Gly Ser Met Leu Asn Glu His Val Cys Ser Val Ile Arg
228 210 215 220
229 Lys Phe Gly Ser Arg Asn Leu Gln Ala Thr Thr Ile Ile Lys Leu Ser
230 225 230 235 240
231 Gln Lys Leu Thr Glu Ala Asn Phe Thr Glu Ile Gln Lys Leu Ala Leu
232 245 250 255
233 Asp Val Ala His Ile His Glu Glu Cys Cys Gln Gly Asn Ser Leu Glu
234 260 265 270
235 Cys Leu Gln Asp Gly Glu Lys Val Met Thr Tyr Ile Cys Ser Gln Gln
236 275 280 285
237 Asn Ile Leu Ser Ser Lys Ile Ala Glu Cys Cys Lys Leu Pro Met Ile
238 290 295 300
239 Gln Leu Gly Phe Cys Ile Ile His Ala Glu Asn Gly Val Lys Pro Glu
240 305 310 315 320
241 Gly Leu Ser Leu Asn Pro Ser Gln Phe Leu Gly Asp Arg Asn Phe Ala
242 325 330 335
243 Gln Phe Ser Ser Glu Glu Lys Ile Met Phe Met Ala Ser Phe Leu His
244 340 345 350
245 Glu Tyr Ser Arg Thr His Pro Asn Leu Pro Val Ser Val Ile Leu Arg
246 355 360 365
247 Ile Ala Lys Thr Tyr Gln Glu Ile Leu Glu Lys Cys Ser Gln Ser Gly

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